

JUL 08 2002

TECH CENTER 1600/2900



1645

RAW SEQUENCE LISTING
PATENT APPLICATION: US/08/325,278A

DATE: 06/10/2002
TIME: 16:22:34

Input Set : A:\402.app
Output Set: N:\CRF3\06102002\H325278A.raw

SEQUENCE LISTING

ENTERED

4 (1) GENERAL INFORMATION:

C--> 6 (i) APPLICANT: Bjorck, Lars
7 Sjobring, Ulf
9 (ii) TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
11 (iii) NUMBER OF SEQUENCES: 15
13 (iv) CORRESPONDENCE ADDRESS:
14 (A) ADDRESSEE: Seed IP Law Group
15 (B) STREET: 701 Fifth Avenue Suite 6300
16 (C) CITY: Seattle
17 (D) STATE: Washington
18 (E) COUNTRY: USA
19 (F) ZIP: 98104-7092
21 (v) COMPUTER READABLE FORM:
22 (A) MEDIUM TYPE: Floppy disk
23 (B) COMPUTER: IBM PC compatible
24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
27 (vi) CURRENT APPLICATION DATA:
C--> 28 (A) APPLICATION NUMBER: US/08/325,278A
C--> 29 (B) FILING DATE: 26-Oct-1994
30 (C) CLASSIFICATION:
32 (viii) ATTORNEY/AGENT INFORMATION:
33 (A) NAME: Potter, Jane E. R.
34 (B) REGISTRATION NUMBER: 33,332
35 (C) REFERENCE/DOCKET NUMBER: 100084.402
37 (ix) TELECOMMUNICATION INFORMATION:
38 (A) TELEPHONE: (206) 622-4900
39 (B) TELEFAX: (206) 682-6031
42 (2) INFORMATION FOR SEQ ID NO: 1:
44 (i) SEQUENCE CHARACTERISTICS:
45 (A) LENGTH: 305 amino acids
46 (B) TYPE: amino acid
47 (C) STRANDEDNESS: unknown
48 (D) TOPOLOGY: unknown
50 (ii) MOLECULE TYPE: protein
52 (iii) HYPOTHETICAL: NO
54 (vi) ORIGINAL SOURCE:
55 (A) ORGANISM: Escherichia coli LE392/pHDL, DSM 7054
59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
61 Ala Val Glu Asn Lys Glu Glu Thr Pro Glu Thr Pro Glu Thr Asp Ser
62 1 5 10 15
64 Glu Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Phe Ala Asn Gly Ser

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65 20 25 30
 67 Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Lys Ala Thr Ser Glu
 68 35 40 45
 70 Ala Tyr Ala Tyr Ala Asp Thr Leu Lys Lys Asn Gly Glu Tyr Thr
 71 50 55 60
 73 Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly
 74 65 70 75 80
 76 Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
 77 85 90 95
 79 Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
 80 100 105 110
 82 Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu
 83 115 120 125
 85 Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr
 86 130 135 140
 88 Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys Thr Pro Glu Glu Pro
 89 145 150 155 160
 91 Lys Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Tyr Ala Asp Gly Lys
 92 165 170 175
 94 Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu
 95 180 185 190
 97 Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Glu Asn Gly Lys Tyr Thr
 98 195 200 205
 100 Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly
 101 210 215 220
 103 Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
 104 225 230 235 240
 106 Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
 107 245 250 255
 109 Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu
 110 260 265 270
 112 Ala Lys Glu Asn Gly Lys Tyr Thr Ala Asp Leu Glu Asp Gly Gly Tyr
 113 275 280 285
 115 Thr Ile Asn Ile Arg Phe Ala Gly Lys Lys Val Asp Glu Lys Pro Glu
 116 290 295 300
 118 Glu
 119 305

121 (2) INFORMATION FOR SEQ ID NO: 2:
 123 (i) SEQUENCE CHARACTERISTICS:
 124 (A) LENGTH: 921 base pairs
 125 (B) TYPE: nucleic acid
 126 (C) STRANDEDNESS: double
 127 (D) TOPOLOGY: unknown
 129 (ii) MOLECULE TYPE: DNA (genomic)
 131 (iii) HYPOTHETICAL: NO
 133 (vi) ORIGINAL SOURCE:
 134 (A) ORGANISM: Escherichia coli LE392/pHDL, DSM 7054
 138 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 140 GCGGTAGAAA ATAAAGAAGA AACACCAGAA ACACCAGAAA CTGATTAGA AGAAGAAGTA

60

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142	ACAATCAAAG CTAACCTAAT CTTTGCAAAT GGAAGCACAC AAACTGCAGA ATTCAAAGGA	120
144	ACATTTGAAA AAGCAACATC AGAAGCTTAT GCGTATGCAG ATACTTTGAA GAAAGACAAT	180
146	GGAGAATATA CTGTAGATGT TGCAAGATAAA GGTTATACTT TAAATATTAA ATTTGCTGGA	240
148	AAAGAAAAAA CACCAGAAGA ACCAAAAGAA GAAGTTACTA TTAAAGCAAA CTTAATCTAT	300
150	GCAGATGGAA AAACACAAAC AGCAGAATTC AAAGGAACAT TTGAAGAAGC AACAGCAGAA	360
152	GCATACAGAT ATGCAGATGC ATTAAGAAG GACAATGGAG AATATACAGT AGACGTTGCA	420
154	GATAAAGGT ATACTTAAA TATTAATTT GCTGGAAAAG AAAAAACACC AGAAGAACCA	480
156	AAAGAAGAAG TTACTATTAA AGCAAACCTA ATCTATGCAG ATGGAAAAAC ACAAACAGCA	540
158	GAATTCAAAG GAACATTGAA AGAAGCAACA GCAGAAGCAT ACAGATATGC TGACTTATTA	600
160	GCAAAAGAAA ATGGTAAATA TACAGTAGAC GTTGCAGATA AAGGTTATAC TTTAAATATT	660
162	AAATTTGCTG GAAAAGAAAA AACACCAGAA GAACCAAAAG AAGAAGTTAC TATTAAGCA	720
164	AACTTAATCT ATGCAGATGG AAAACTCAA ACAGCAGAGT TCAAAGGAAC ATTTGCAGAA	780
166	GCAACAGCAG AAGCATACAG ATACGCTGAC TTATTAGCAA AAGAAAATGG TAAATATACA	840
168	GCAGACTTAG AAGATGGTGG ATACACTATT AATATTAGAT TTGCAGGTAA GAAAGTTGAC	900
170	AAAAAACCAG AAGAATAATA A	921

172 (2) INFORMATION FOR SEQ ID NO: 3:

174 (i) SEQUENCE CHARACTERISTICS:
175 (A) LENGTH: 434 amino acids
176 (B) TYPE: amino acid
177 (C) STRANDEDNESS: unknown
178 (D) TOPOLOGY: unknown
180 (ii) MOLECULE TYPE: protein
182 (iii) HYPOTHETICAL: NO
184 (vi) ORIGINAL SOURCE:

185 (A) ORGANISM: Escherichia coli LE392/pHDLG, DSM 7055

189	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
191	Ala Val Glu Asn Lys Glu Glu Thr Pro Glu Thr Pro Glu Thr Asp Ser
192	1 5 10 15
194	Glu Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Phe Ala Asn Gly Ser
195	20 25 30
197	Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Lys Ala Thr Ser Glu
198	35 40 45
200	Ala Tyr Ala Tyr Ala Asp Thr Leu Lys Lys Asp Asn Gly Glu Tyr Thr
201	50 55 60
203	Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly
204	65 70 75 80
206	Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Val Thr Ile Lys Ala
207	85 90 95
209	Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
210	100 105 110
212	Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu
213	115 120 125
215	Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr
216	130 135 140
218	Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys Thr Pro Glu Glu Pro
219	145 150 155 160
221	Lys Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Tyr Ala Asp Gly Lys
222	165 170 175
224	Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu

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225	180	185	190	
227	Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Glu Asn Gly Lys Tyr Thr			
228	195	200	205	
229	Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly			
230	210	215	220	
231				
232	Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala			
233	225	230	235	240
234				
235	Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly			
236	245	250	255	
237				
238	Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu			
239	260	265	270	
240				
241	Ala Lys Glu Asn Gly Lys Tyr Thr Ala Asp Leu Glu Asp Gly Gly Tyr			
242	275	280	285	
243				
244	Thr Ile Asn Ile Arg Phe Ala Gly Lys Lys Val Asp Glu Lys Pro Glu			
245	290	295	300	
246				
247	Glu Pro Met Asp Thr Tyr Lys Leu Ile Leu Asn Gly Lys Thr Leu Lys			
248	305	310	315	320
249				
250	Gly Glu Thr Thr Glu Ala Val Asp Ala Ala Thr Ala Glu Lys Val			
251	325	330	335	
252				
253	Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val Asp Gly Glu Trp Thr Tyr			
254	340	345	350	
255				
256	Asp Asp Ala Thr Lys Thr Phe Thr Val Thr Glu Lys Pro Glu Val Ile			
257	355	360	365	
258				
259	Asp Ala Ser Glu Leu Thr Pro Ala Val Thr Thr Tyr Lys Leu Val Ile			
260	370	375	380	
261				
262	Asn Gly Lys Thr Leu Lys Gly Glu Thr Thr Lys Ala Val Asp Ala			
263	385	390	395	400
264				
265	Glu Thr Ala Glu Lys Ala Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val			
266	405	410	415	
267				
268	Asp Gly Val Trp Thr Tyr Asp Asp Ala Thr Lys Thr Phe Thr Val Thr			
269	420	425	430	
270				

(2) INFORMATION FOR SEO ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1308 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: dou

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: D

iii) HYPOTHETICAL: NO

ORIGINAL SOURCE:

(A) ORGANISM: E

(xi) SEQUENCE DESCRIPT

ATAAAAGAAGA AACACCAGAA ACACCCAGAAA CTTGATTCAGA AGAAGAAT
CTTACGCTATT CTTTCCGAAAT CGAACCGACAG AAGACTCCGACA ATTGAA

CTCAAAG CTAACCTAAI CTTTGCAAAT GGAAGCACAC
TTGCAAA AGGAGATG AGAACCTTAT CGCTTATGGAC

298	ACATTTGAAA	AAGCAACATC	AGAAGCTTAT	GCGTATGCG	ATACATTTGAA	GAAAGACAA	180
300	GGAGAAATATA	CTGTAGATGT	TGCAGATAAA	GGTTATACCT	TAATATTAA	ATTTGCTGGA	240
302	AAAGAAAAAA	CACCAGAAGA	ACCAAAAGAA	GAAGTTACTA	TTAAAGCAAA	CTTAATCTAT	300
304	GCAGATGGAA	AAACACAAAC	AGCAGAATT	AAAGGAACAT	TTGAAGAAC	AACAGCAGAA	360

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306	GCATACAGAT	ATGCAGATGC	ATTAAAGAAG	GACAATGGAG	AATATACAGT	AGACGTTGCA	420
308	GATAAAGGTT	ATACTTTAAA	TATTAAATT	GCTGAAAAG	AAAAAACACC	AGAAGAACCA	480
310	AAAGAAGAAG	TTACTATTAA	AGCAAACCTA	ATCTATGCAG	ATGGAAAAAC	ACAAACAGCA	540
312	GAATTCAAAG	GAACATTTGA	AGAAGCAACA	GCAGAAGCAT	ACAGATATGC	TGACTTATT	600
314	GCAAAAGAAA	ATGGTAAATA	TACAGTAGAC	GTTGCAGATA	AAGGTTATAC	TTTAAATATT	660
316	AAATTTGCTG	AAAAAGAAAA	AACACCAGAA	GAACCAAAG	AAGAAGTTAC	TATTAAGCA	720
318	AACTTAATCT	ATGCAGATGG	AAAAACTCAA	ACAGCAGAGT	TCAAAGGAAC	ATTGCAGAA	780
320	GCAACAGCAG	AAGCATACAG	ATACGCTGAC	TTATTAGCAA	AAGAAAATGG	TAAATATACA	840
322	GCAGACTTAG	AAGATGGTGG	ATACACTATT	AATATTAGAT	TTGCAGGTAA	GAAAGTTGAC	900
324	GAAAAACCGAG	AAGAACCCAT	GGACACTTAC	AAATTAATCC	TTAATGGTAA	AACATTGAAA	960
326	GGCGAAACAA	CTACTGAAGC	TGTTGATGCT	GCTACTGCAG	AAAAAGTCTT	CAAACAATAC	1020
328	GCTAACGACA	ACGGTGTGTA	CGGTGAATGG	ACTTACGACG	ATGCGACTAA	GACCTTTACA	1080
330	GTTACTGAAA	AACCAGAAGT	GATCGATGCG	TCTGAATTAA	CACCAGCCGT	GACAACATTAC	1140
332	AAACTTGTAA	TTAATGGTAA	AACATTGAAA	GGCGAAACAA	CTACTAAAGC	AGTAGACGCA	1200
334	GAAACTGCAG	AAAAAGCCTT	CAAACAATAC	GCTAACGACA	ACGGTGTGTA	TGGTGTGTTGG	1260
336	ACTTATGATG	ATGCAGACTAA	GACCTTTACG	GTAACTGAAA	TGTAATAAA		1308

338 (2) INFORMATION FOR SEQ ID NO: 5:

340 (i) SEQUENCE CHARACTERISTICS:

341	(A) LENGTH: 1332 base pairs
342	(B) TYPE: nucleic acid
343	(C) STRANDEDNESS: double
344	(D) TOPOLOGY: unknown

346 (ii) MOLECULE TYPE: DNA (genomic)

348 (iii) HYPOTHETICAL: NO

351 (ix) FEATURE:

352	(A) NAME/KEY: CDS
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353	(B) LOCATION: 1..1329
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356 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

358	AAC GGT GAT GGT AAT CCT AGG GAA GTT ATA GAA GAT CTT GCA GCA AAC	48
359	Asn Gly Asp Gly Asn Pro Arg Glu Val Ile Glu Asp Leu Ala Ala Asn	
360	1 5 10 15	
362	AAT CCC GCA ATA CAA AAT ATA CGT TTA CGT CAC GAA AAC AAG GAC TTA	96
363	Asn Pro Ala Ile Gln Asn Ile Arg Leu Arg His Glu Asn Lys Asp Leu	
364	20 25 30	
366	AAA GCG AGA TTA GAG AAT GCA ATG GAA GTT GCA GGA AGA GAT TTT AAG	144
367	Lys Ala Arg Leu Glu Asn Ala Met Glu Val Ala Gly Arg Asp Phe Lys	
368	35 40 45	
370	AGA GCT GAA GAA CTT GAA AAA GCA AAA CAA GCC TTA GAA GAC CAG CGT	192
371	Arg Ala Glu Glu Leu Glu Lys Ala Lys Gln Ala Leu Glu Asp Gln Arg	
372	50 55 60	
374	AAA GAT TTA GAA ACT AAA TTA AAA GAA CTA CAA CAA GAC TAT GAC TTA	240
375	Lys Asp Leu Glu Thr Lys Leu Lys Glu Leu Gln Gln Asp Tyr Asp Leu	
376	65 70 75 80	
378	GCA AAG GAA TCA ACA AGT TGG GAT AGA CAA AGA CTT GAA AAA GAG TTA	288
379	Ala Lys Glu Ser Thr Ser Trp Asp Arg Gln Arg Leu Glu Lys Glu Leu	
380	85 90 95	
382	GAA GAG AAA AAG GAA GCT CTT GAA TTA GCG ATA GAC CAG GCA AGT CGG	336
383	Glu Glu Lys Lys Glu Ala Leu Glu Leu Ala Ile Asp Gln Ala Ser Arg	
384	100 105 110	

VERIFICATION SUMMARY

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Input Set : A:\402.app

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L:6 M:220 C: Keyword misspelled or invalid format, [(i) APPLICANT:]

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]